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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/451,527

DATE: 12/16/1999  
TIME: 16:05:39

Input Set: I451527.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

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1 <110> APPLICANT: Sim, Gek-Kee
2      Yang, Shumin
3      Dreitz, Matthew J.
4      Wonderling, Ramani S.
5 <120> TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
6      ACID MOLECULES, AND USES THEREOF
7 <130> FILE REFERENCE: IM-2-C2
8 <140> CURRENT APPLICATION NUMBER: US/09/451,527
9 <141> CURRENT FILING DATE: 1999-12-01
10 <150> EARLIER APPLICATION NUMBER: 09/322,409
11 <151> EARLIER FILING DATE: 1999-05-28
12 <150> EARLIER APPLICATION NUMBER: 60/087,306
13 <151> EARLIER FILING DATE: 1998-05-29
14 <160> NUMBER OF SEQ ID NOS: 174
15 <170> SOFTWARE: PatentIn Ver. 2.0
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18 <212> TYPE: DNA
19 <213> ORGANISM: Canis familiaris
20 <220> FEATURE:
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25                                     Met Gly Leu Thr
26                                     1
27      tcc caa ctg att cca act ctg gtc tgc tta cta gca ctc acc agc acc      102
28      Ser Gln Leu Ile Pro Thr Leu Val Cys Leu Leu Ala Leu Thr Ser Thr
29      5              10              15              20
30      ttt gtc cac gga cat aac ttc aat att act att aaa gag atc atc aaa      150
31      Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys Glu Ile Ile Lys
32      25              30              35
33      atg ttg aac atc ctc aca gcg aga aac gac tcg tgc atg gag ctg act      198
34      Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr
35      40              45              50
36      gtc aag gac gtc ttc act gct cca aag aac aca agc gat aag gaa atc      246
37      Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile
38      55              60              65
39      ttc tgc aga gct gct act gta ctg cgg cag atc tat aca cac aac tgc      294
40      Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys
41      70              75              80
42      tcc aac aga tat ctc aga gga ctc tac agg aac ctc agc agc atg gca      342
43      Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala
44      85              90              95              100
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45      aac aag acc tgt tct atg aat gaa atc aag aag agt aca ctg aaa gac      390
46      Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp
47              105                      110                      115
48      ttc ttg gaa agg cta aaa gtg atc atg cag aag aaa tac tac agg cat      438
49      Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
50              120                      125                      130
51      tgaagctgaa tattttaatt tatgagtttt taaatagctt tattttaaaa atattttatat 498
52      atttataaca taataaaaata aaatatatat agaaaaaaaa aaaaaaaaaa a      549

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&lt;210&gt; SEQ ID NO 2

&lt;211&gt; LENGTH: 132

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Canis familiaris

&lt;400&gt; SEQUENCE: 2

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58      Met Gly Leu Thr Ser Gln Leu Ile Pro Thr Leu Val Cys Leu Leu Ala
59      1              5              10              15
60      Leu Thr Ser Thr Phe Val His Gly His Asn Phe Asn Ile Thr Ile Lys
61              20              25              30
62      Glu Ile Ile Lys Met Leu Asn Ile Leu Thr Ala Arg Asn Asp Ser Cys
63              35              40              45
64      Met Glu Leu Thr Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser
65      50              55              60
66      Asp Lys Glu Ile Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr
67      65              70              75              80
68      Thr His Asn Cys Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu
69              85              90              95
70      Ser Ser Met Ala Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser
71              100              105              110
72      Thr Leu Lys Asp Phe Leu Glu Arg Leu Lys Val Ile Met Gln Lys Lys
73              115              120              125
74      Tyr Tyr Arg His
75      130

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&lt;210&gt; SEQ ID NO 3

&lt;211&gt; LENGTH: 549

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Canis familiaris

&lt;400&gt; SEQUENCE: 3

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81      tttttttttt tttttttttt tatatatatt ttatttttatt atgtttataaa tatataaata 60
82      tttttaaaat aaagctatatt aaaaactcat aaatttaaaat attcagcttc aatgcctgta 120
83      gtatttcttc tgcgatgaca ctttttagcct ttccaagaag tcttttcagt tactcttctt 180
84      gatttcattc atagaacagg tcttggttgc catgctgctg aggttcctgt agagtcctct 240
85      gagatatctg ttggagcagt tgtgtgtata gatctgccgc agtacagtag cagctctgca 300
86      gaagatttcc ttatcgcttg tggtcttttg agcagtgaag acgtccttga cagtcagctc 360
87      catgcacgag tcgtttctcg ctgtgaggat gttcaacatt ttgatgatct ctttaatagt 420
88      aatattgaag ttatgtccgt ggacaaaggt gctggtgagt gctagtaagc agaccagagt 480
89      tggaatcagt tgggaggtga gaccattaa tagatctcta tttgcagtga caatagcaga 540
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90      549

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&lt;210&gt; SEQ ID NO 4

&lt;211&gt; LENGTH: 396

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Canis familiaris

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/451,527

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98      ctcacagcga gaaacgactc gtgcatggag ctgactgtca aggacgtctt cactgctcca 180
99      aagaacacaa gcgataagga aatcttctgc agagctgcta ctgtactgcg gcagatctat 240
100     acacacaact gctccaacag atatctcaga ggactctaca ggaacctcag cagcatggca 300
101     aacaagacct gttctatgaa tgaaatcaag aagagtacac tgaaagactt cttggaaagg 360
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105  <212> TYPE: DNA
106  <213> ORGANISM: Canis familiaris
107  <400> SEQUENCE: 5
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109      actcttcttg atttcattca tagaacaggt cttgtttgcc atgctgctga gggtcctgta 120
110      gagtcctctg agatatctgt tggagcagtt gtgtgtatag atctgccgca gtacagtagc 180
111      agctctgcag aagatttctt tatcgtctgt gttctttgga gcagtgaaga cgctccttgac 240
112      agtcagctcc atgcacgagt cgtttctcgc tgtgaggatg ttcaacattt tgatgatctc 300
113      tttaatatga atattgaagt tatgtccgtg gacaaagggtg ctggtgagtg ctagtaagca 360
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118  <213> ORGANISM: Canis familiaris
119  <220> FEATURE:
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121  <222> LOCATION: (35)..(916)
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124                                     Met Ile Val Leu Ala Pro Ala
125                                     1           5
126      tgg agc cca act gcc tcc ctg ttg ctg ctg ctg ctg ctc agc ccc ggc 103
127      Trp Ser Pro Thr Ala Ser Leu Leu Leu Leu Leu Leu Leu Ser Pro Gly
128               10           15           20
129      ctc cgc ggg acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc 151
130      Leu Arg Gly Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser
131               25           30           35
132      acc ttc gcg gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac 199
133      Thr Phe Ala Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp
134               40           45           50           55
135      tat cca gtc act gtc gcc tcc aac ctg cag gac gac gag ctc tgc ggg 247
136      Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly
137               60           65           70
138      gcg ttc tgg cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag 295
139      Ala Phe Trp Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln
140               75           80           85
141      gct gtg gct gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg 343
142      Ala Val Ala Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr
143               90           95           100
144      gag ata cac ttt gtc acc ttc tgt gcc ttc cag ccc ctc ccc agc tgt 391

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145	Glu Ile His Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys	
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147	ctt cgc ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc	439
148	Leu Arg Phe Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser	
149	120 125 130 135	
150	cag cag ctg gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc	487
151	Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser	
152	140 145 150	
153	ggg tgc ctg gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc	535
154	Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro	
155	155 160 165	
156	cca agg agc ccc ggg gcc ctg gag gcc act gcc ttg cca gcc cct cag	583
157	Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln	
158	170 175 180	
159	gca cct cgg ctg ctc ctc ctg ctg ctg ctg ccc gtg gct ctc ctg ctg	631
160	Ala Pro Arg Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu	
161	185 190 195	
162	atg tcc act gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg	679
163	Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Arg	
164	200 205 210 215	
165	tca ccc tac cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc	727
166	Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser	
167	220 225 230	
168	cat ctg ccc gag gac aca gag ctg gga cct gga ggg agt cag cta gag	775
169	His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu	
170	235 240 245	
171	act ggt ccc ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga	823
172	Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly	
173	250 255 260	
174	tca agg caa cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca	871
175	Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro	
176	265 270 275	
177	cct ctc ccc ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata	916
178	Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile	
179	280 285 290	
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188	1 5 10 15	
189	Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro Asp Cys Ser Phe	
190	20 25 30	
191	Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu	
192	35 40 45	
193	Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu	
194	50 55 60	

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195      Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln
196      65                      70                      75                      80
197      Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
198                      85                      90                      95
199      Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
200                      100                      105                      110
201      Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
202                      115                      120                      125
203      His Leu Leu Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp
204                      130                      135                      140
205      Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
206      145                      150                      155                      160
207      Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala
208                      165                      170                      175
209      Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Leu
210                      180                      185                      190
211      Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp
212                      195                      200                      205
213      Arg Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr
214                      210                      215                      220
215      Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly
216      225                      230                      235                      240
217      Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala
218                      245                      250                      255
219      Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro
220                      260                      265                      270
221      Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu
222                      275                      280                      285
223      Pro Pro Arg Asn Cys Ile
224                      290
225      <210> SEQ ID NO 8
226      <211> LENGTH: 1013
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232      actttgtaca gagggggaga ggtggggctg gggctggctt tgggggctgt gggggcgggc 180
233      gttgccttga tcctggggag ggagcgagcg gggctgcgtg gtcgaggaag ggaccagtct 240
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235      gcctcagtgt cctctgctcc ccagggtagg gtgacctccg ccgccgcctc cttcgccaat 360
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237      gccgaggtgc ctgaggggct ggcaaggcag tggcctccag ggccccgggg ctccctgggg 480
238      gcaccaatgt agaggagtcg ggctgacact gcagctccag gcacccggag aaattcctgc 540
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VERIFICATION SUMMARY  
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DATE: 12/16/1999  
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Original Text

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